CONSIDER FOR TALK

9th Annual SEA-PHAGES Symposium Abstract

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Comparative genomic analysis and genome annotation of mycobacteriophages AFIS and JewelBug

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Mycobacteriophages AFIS (A1) and JewelBug (A6) were isolated in Fall 2014 and Fall 2012 and selected for genome annotation in Spring 2017. Putative genes were called using the bioinformatics tools DNA Master, Glimmer, GeneMark, BLAST and Phamerator. Functions of the putative gene products were assigned based on homology to previously characterized proteins programs BLAST, HHPred and Phamerator and PECAAN was used for a quality control analysis of the final genome annotation file. Most annotated gene functions were associated with structure, replication and protection of the mycobacteriophage genetic material. Two frameshift mutations were annotated through comparative genomic analysis. One frameshift mutation was annotated in JewelBug using comparison with the tapemeasure protein for phage Jeffabunny. An additional frameshift mutation was annotated through comparison of gene 23 in AFIS and similar genes found in CactusRose, Wheeler, Bigfoot and Graduation, phages in subcluster A1. Gene products with unknown function were also investigated using I-TASSER. Putative protein functions based on homology of protein structure by predictive structural analysis included Beta-lactamase, DNA helicase, immunity repressor, DNA and RNA polymerase, nuclease enzymes, peptidase, thioredoxin.

Seventy three phage genomes isolated from Purdue were also sequenced by Purdue Genomics Core Facility through WideSeq service. The sequenced genomes will be annotated and analyzed together with peptide data obtained using mass spectrometry. Studies have shown that GC content of mycobacteriophage genomes ranges from 50.3% to 70% and mycobacteriophages from the same cluster have similar GC content. GC content analysis will be conducted on sequenced phage genomes to examine potential correlations between the genes in the mycobacteriophage genomes and the host Mycobacterium smegmatis (M. smegmatis).

The identification of putative antibiotic resistance proteins in annotated phage AFIS suggests that mycobacteriophage could provide an alternative pathway for the spread of antibiotic resistance through a bacterial community by phage infection and replication. The GC content of AFIS, M. smegmatis, and M. tuberculosis are similar and suggests that this putative alternative pathway could provide an example of bacteriophages acting as a double-edged sword: some phages may lyse and kill the bacteria, while others may increase the virulence of bacteria. Further research into bacteriophages and their protein functions is paramount for working towards applying phage therapy in medical practice. Future collaborative work includes identification of priority candidates for determination of protein structure through wet lab experiments in the classroom.